

RAW SEQUENCE LISTING

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Application Serial Number: 10/788,489
Source: IFWO
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RAW SEQUENCE LISTING

DATE: 04/12/2006

PATENT APPLICATION: US/10/788,489

TIME: 12:28:49

Input Set : N:\Crf3\RULE60\10788489.raw

Output Set: N:\CRF4\04122006\J788489.raw

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1 <110> APPLICANT: CARILLO, Serge
2     BLANCHARD, Jean-Marie
3     PIECHACZYK, Marc
4 <120> TITLE OF INVENTION: METHOD OF CANCER TREATMENT BY P53 PROTEIN CONTROL
5 <130> FILE REFERENCE: ST94037A-US
6 <140> CURRENT APPLICATION NUMBER: US/10/788,489
7 <141> CURRENT FILING DATE: 2004-03-01
8 <150> PRIOR APPLICATION NUMBER: US/09/405,920
9 <151> PRIOR FILING DATE: 1999-09-24
10 <150> PRIOR APPLICATION NUMBER: 08/737,953
11 <151> PRIOR FILING DATE: 1996-11-27
12 <150> PRIOR APPLICATION NUMBER: FR94/06583
13 <151> PRIOR FILING DATE: 1994-05-31
14 <150> PRIOR APPLICATION NUMBER: WO PCT/FR95/00670
15 <151> PRIOR FILING DATE: 1995-05-22
16 <160> NUMBER OF SEQ ID NOS: 4
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 2085
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (1)..(2085)
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30     gta aaa aca gaa cct gag aag aag tca cag tca acc aag ctg tct gtg      96
31     Val Lys Thr Glu Pro Glu Lys Lys Ser Gln Ser Thr Lys Leu Ser Val
32             20             25             30
33     gtt cat gag aaa aaa tcc caa gaa gga aag cca aaa gaa cac aca gag      144
34     Val His Glu Lys Lys Ser Gln Glu Gly Lys Pro Lys Glu His Thr Glu
35             35             40             45
36     cca aaa agc cta ccc aag cag gca tca gat aca gga agt aac gat gct      192
37     Pro Lys Ser Leu Pro Lys Gln Ala Ser Asp Thr Gly Ser Asn Asp Ala
38             50             55             60
39     cac aat aaa aaa gca gtt tcc aga tca gct gaa cag cag cca tca gag      240
40     His Asn Lys Lys Ala Val Ser Arg Ser Ala Glu Gln Gln Pro Ser Glu
41             65             70             75             80
42     aaa tca aca gaa cca aag act aaa cca caa gac atg att tct gct ggt      288
43     Lys Ser Thr Glu Pro Lys Thr Lys Pro Gln Asp Met Ile Ser Ala Gly
44             85             90             95

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45	gga gag agt gtt gct ggt atc act gca ata tct ggc aag ccg ggt gac	336
46	Gly Glu Ser Val Ala Gly Ile Thr Ala Ile Ser Gly Lys Pro Gly Asp	
47	100 105 110	
48	aag aaa aaa gaa aag aaa tca tta acc cca gct gtg cca gtt gaa tct	384
49	Lys Lys Lys Glu Lys Lys Ser Leu Thr Pro Ala Val Pro Val Glu Ser	
50	115 120 125	
51	aaa ccg gat aaa cca tcg gga aag tca ggc atg gat gct gct ttg gat	432
52	Lys Pro Asp Lys Pro Ser Gly Lys Ser Gly Met Asp Ala Ala Leu Asp	
53	130 135 140	
54	gac tta ata gat act tta gga gga cct gaa gaa act gaa gaa gaa aat	480
55	Asp Leu Ile Asp Thr Leu Gly Gly Pro Glu Glu Thr Glu Glu Glu Asn	
56	145 150 155 160	
57	aca acg tat act gga cca gaa gtt tca gat cca atg agt tcc acc tac	528
58	Thr Thr Tyr Thr Gly Pro Glu Val Ser Asp Pro Met Ser Ser Thr Tyr	
59	165 170 175	
60	ata gag gaa ttg ggt aaa aga gaa gtc aca att cct cca aaa tat agg	576
61	Ile Glu Glu Leu Gly Lys Arg Glu Val Thr Ile Pro Pro Lys Tyr Arg	
62	180 185 190	
63	gaa cta ttg gct aaa aag gaa ggg atc aca ggg cct cct gca gac tct	624
64	Glu Leu Leu Ala Lys Lys Glu Gly Ile Thr Gly Pro Pro Ala Asp Ser	
65	195 200 205	
66	tca aaa ccc ata ggg cca gat gat gct ata gac gcc ttg tca tct gac	672
67	Ser Lys Pro Ile Gly Pro Asp Asp Ala Ile Asp Ala Leu Ser Ser Asp	
68	210 215 220	
69	ttc acc tgt ggg tcg cct aca gct gct gga aag aaa act gaa aaa gag	720
70	Phe Thr Cys Gly Ser Pro Thr Ala Ala Gly Lys Lys Thr Glu Lys Glu	
71	225 230 235 240	
72	gaa tct aca gaa gtt tta aaa gct cag tca gca ggg aca gtc aga agt	768
73	Glu Ser Thr Glu Val Leu Lys Ala Gln Ser Ala Gly Thr Val Arg Ser	
74	245 250 255	
75	gct gct cca ccc caa gag aag aaa aga aag gtg gag aag gat aca atg	816
76	Ala Ala Pro Pro Gln Glu Lys Lys Arg Lys Val Glu Lys Asp Thr Met	
77	260 265 270	
78	agt gat caa gca ctc gag gct ctg tcg gct tca ctg ggc acc cgg caa	864
79	Ser Asp Gln Ala Leu Glu Ala Leu Ser Ala Ser Leu Gly Thr Arg Gln	
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81	gca gaa cct gag ctc gac ctc cgc tca att aag gaa gtc gat gag gca	912
82	Ala Glu Pro Glu Leu Asp Leu Arg Ser Ile Lys Glu Val Asp Glu Ala	
83	290 295 300	
84	aaa gct aaa gaa gaa aaa cta gag aag tgt ggt gag gat gat gaa aca	960
85	Lys Ala Lys Glu Glu Lys Leu Glu Lys Cys Gly Glu Asp Asp Glu Thr	
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87	atc cca tct gag tac aga tta aaa cca gcc acg gat aaa gat gga aaa	1008
88	Ile Pro Ser Glu Tyr Arg Leu Lys Pro Ala Thr Asp Lys Asp Gly Lys	
89	325 330 335	
90	cca cta ttg cca gag cct gaa gaa aaa ccc aag cct cgg agt gaa tca	1056
91	Pro Leu Leu Pro Glu Pro Glu Glu Lys Pro Lys Pro Arg Ser Glu Ser	
92	340 345 350	
93	gaa ctc att gat gaa ctt tca gaa gat ttt gac cgg tct gaa tgt aaa	1104

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94	Glu Leu Ile Asp Glu Leu Ser Glu Asp Phe Asp Arg Ser Glu Cys Lys	
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96	gag aaa cca tct aag cca act gaa aag aca gaa gaa tct aag gcc gct	1152
97	Glu Lys Pro Ser Lys Pro Thr Glu Lys Thr Glu Glu Ser Lys Ala Ala	
98	370 375 380	
99	gct cca gct cct gtg tcg gag gct gtg tct cgg acc tcc atg tgt agt	1200
100	Ala Pro Ala Pro Val Ser Glu Ala Val Ser Arg Thr Ser Met Cys Ser	
101	385 390 395 400	
102	ata cag tca gca ccc cct gag ccg gct acc ttg aag ggc aca gtg cca	1248
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104	405 410 415	
105	gat gat gct gta gaa gcc ttg gct gat agc ctg ggg aaa aag gaa gca	1296
106	Asp Asp Ala Val Glu Ala Leu Ala Asp Ser Leu Gly Lys Lys Glu Ala	
107	420 425 430	
108	gat cca gaa gat gga aaa cct gtg atg gat aaa gtc aag gag aag gcc	1344
109	Asp Pro Glu Asp Gly Lys Pro Val Met Asp Lys Val Lys Glu Lys Ala	
110	435 440 445	
111	aaa gaa gaa gac cgt gaa aag ctt ggt gaa aaa gaa gaa aca att cct	1392
112	Lys Glu Glu Asp Arg Glu Lys Leu Gly Glu Lys Glu Glu Thr Ile Pro	
113	450 455 460	
114	cct gat tat aga tta gaa gag gtc aag gat aaa gat gga aag cca ctc	1440
115	Pro Asp Tyr Arg Leu Glu Glu Val Lys Asp Lys Asp Gly Lys Pro Leu	
116	465 470 475 480	
117	ctg cca aaa gag tct aag gaa cag ctt cca ccc atg agt gaa gac ttc	1488
118	Leu Pro Lys Glu Ser Lys Glu Gln Leu Pro Pro Met Ser Glu Asp Phe	
119	485 490 495	
120	ctt ctg gat gct ttg tct gag gac ttc tct ggt cca caa aat gct tca	1536
121	Leu Leu Asp Ala Leu Ser Glu Asp Phe Ser Gly Pro Gln Asn Ala Ser	
122	500 505 510	
123	tct ctt aaa ttt gaa gat gct aaa ctt gct gct gcc atc tct gaa gtg	1584
124	Ser Leu Lys Phe Glu Asp Ala Lys Leu Ala Ala Ala Ile Ser Glu Val	
125	515 520 525	
126	gtt tcc caa acc cca gct tca acg acc caa gct gga gcc cca ccc cgt	1632
127	Val Ser Gln Thr Pro Ala Ser Thr Thr Gln Ala Gly Ala Pro Pro Arg	
128	530 535 540	
129	gat acc tcg cag agt gac aaa gac ctc gat gat gcc ttg gat aaa ctc	1680
130	Asp Thr Ser Gln Ser Asp Lys Asp Leu Asp Asp Ala Leu Asp Lys Leu	
131	545 550 555 560	
132	tct gac agt cta gga caa agg cag cct gac cca gat gag aac aaa cca	1728
133	Ser Asp Ser Leu Gly Gln Arg Gln Pro Asp Pro Asp Glu Asn Lys Pro	
134	565 570 575	
135	atg gga gat aaa gta aag gaa aaa gct aaa gct gaa cat aga gac aag	1776
136	Met Gly Asp Lys Val Lys Glu Lys Ala Lys Ala Glu His Arg Asp Lys	
137	580 585 590	
138	ctt gga gaa aga gat gac act atc cca cct gaa tac aga cat ctc ctg	1824
139	Leu Gly Glu Arg Asp Asp Thr Ile Pro Pro Glu Tyr Arg His Leu Leu	
140	595 600 605	
141	gat gat aat gga cag gac aaa cca gtg aag cca cct aca aag aaa tca	1872
142	Asp Asp Asn Gly Gln Asp Lys Pro Val Lys Pro Pro Thr Lys Lys Ser	

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144 gag gat tca aag aaa cct gca gat gac caa gac ccc att gat gct ctc 1920
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146 625          630          635          640
147 tca gga gat ctg gac agc tgt ccc tcc act aca gaa acc tca cag aac 1968
148 Ser Gly Asp Leu Asp Ser Cys Pro Ser Thr Thr Glu Thr Ser Gln Asn
149          645          650          655
150 aca gca aag gat aag tgc aag aag gct gct tcc agc tcc aaa gca cct 2016
151 Thr Ala Lys Asp Lys Cys Lys Lys Ala Ala Ser Ser Ser Lys Ala Pro
152          660          665          670
153 aag aat gga ggt aaa gcg aag gat tca gca aag aca aca gag gaa act 2064
154 Lys Asn Gly Gly Lys Ala Lys Asp Ser Ala Lys Thr Thr Glu Glu Thr
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162 <212> TYPE: PRT
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170          35          40          45
171 Pro Lys Ser Leu Pro Lys Gln Ala Ser Asp Thr Gly Ser Asn Asp Ala
172          50          55          60
173 His Asn Lys Lys Ala Val Ser Arg Ser Ala Glu Gln Gln Pro Ser Glu
174          65          70          75          80
175 Lys Ser Thr Glu Pro Lys Thr Lys Pro Gln Asp Met Ile Ser Ala Gly
176          85          90          95
177 Gly Glu Ser Val Ala Gly Ile Thr Ala Ile Ser Gly Lys Pro Gly Asp
178          100          105          110
179 Lys Lys Lys Glu Lys Lys Ser Leu Thr Pro Ala Val Pro Val Glu Ser
180          115          120          125
181 Lys Pro Asp Lys Pro Ser Gly Lys Ser Gly Met Asp Ala Ala Leu Asp
182          130          135          140
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184          145          150          155          160
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186          165          170          175
187 Ile Glu Glu Leu Gly Lys Arg Glu Val Thr Ile Pro Pro Lys Tyr Arg
188          180          185          190
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190          195          200          205
191 Ser Lys Pro Ile Gly Pro Asp Asp Ala Ile Asp Ala Leu Ser Ser Asp
192          210          215          220

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196					245					250					255	
197	Ala	Ala	Pro	Pro	Gln	Glu	Lys	Lys	Arg	Lys	Val	Glu	Lys	Asp	Thr	Met
198				260					265					270		
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200			275					280					285			
201	Ala	Glu	Pro	Glu	Leu	Asp	Leu	Arg	Ser	Ile	Lys	Glu	Val	Asp	Glu	Ala
202		290					295					300				
203	Lys	Ala	Lys	Glu	Glu	Lys	Leu	Glu	Lys	Cys	Gly	Glu	Asp	Asp	Glu	Thr
204	305					310					315					320
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206				325					330						335	
207	Pro	Leu	Leu	Pro	Glu	Pro	Glu	Glu	Lys	Pro	Lys	Pro	Arg	Ser	Glu	Ser
208				340					345					350		
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210			355					360					365			
211	Glu	Lys	Pro	Ser	Lys	Pro	Thr	Glu	Lys	Thr	Glu	Glu	Ser	Lys	Ala	Ala
212		370					375					380				
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214	385					390					395					400
215	Ile	Gln	Ser	Ala	Pro	Pro	Glu	Pro	Ala	Thr	Leu	Lys	Gly	Thr	Val	Pro
216				405						410					415	
217	Asp	Asp	Ala	Val	Glu	Ala	Leu	Ala	Asp	Ser	Leu	Gly	Lys	Lys	Glu	Ala
218				420					425					430		
219	Asp	Pro	Glu	Asp	Gly	Lys	Pro	Val	Met	Asp	Lys	Val	Lys	Glu	Lys	Ala
220		435					440						445			
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224	465					470					475					480
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226				485						490					495	
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228				500					505					510		
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237	Met	Gly	Asp	Lys	Val	Lys	Glu	Lys	Ala	Lys	Ala	Glu	His	Arg	Asp	Lys
238				580					585					590		
239	Leu	Gly	Glu	Arg	Asp	Asp	Thr	Ile	Pro	Pro	Glu	Tyr	Arg	His	Leu	Leu
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VERIFICATION SUMMARY

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L:158 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1